

Sequence alignment: Hands on

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Move and create a directory

```
cd ~/mda12
```

```
mkdir -p mapping
```

Index reference

```
time bwa index\  
resources/ref/human_g1k_v37.chr20.fasta
```

```
time samtools faidx\  
resources/ref/human_g1k_v37.chr20.fasta
```

Align pair 1

```
time bwa aln -t 1 -l 40 -k 2\  
resources/ref/human_g1k_v37.chr20.fasta\  
resources/data/test_1.fq >\  
mapping/test_1.sai
```

Align pair 2

```
time bwa aln -t 1 -l 40 -k 2\  
resources/ref/human_g1k_v37.chr20.fasta\  
resources/data/test_2.fq >\  
mapping/test_2.sai
```

Mege paired-end in SAM

```
time bwa sampe -n 1\  
resources/ref/human_g1k_v37.chr20.fasta\  
mapping/test_1.sai mapping/test_2.sai\  
resources/data/test_1.fq\  
resources/data/test_2.fq >\  
mapping/test.sam
```

SAM to BAM conversion

```
time samtools view -bS\  
mapping/test.sam -o mapping/test.bam
```

Filter alignment

```
time samtools view -S -h -F 4 -q 10\  
mapping/test.sam | grep -v "XA:Z:" >\  
mapping/test_mapped.sam
```


SAM to BAM conversion

```
time samtools view -bS\  
mapping/test_mapped.sam\  
-o mapping/test_mapped.bam
```

Basic stats all reads

```
time samtools flagstat\  
mapping/test.bam |\  
tee mapping/flagstat_all.txt
```

Basic stats mapped reads

```
time samtools flagstat\  
mapping/test_mapped.bam |\  
tee mapping/flagstat_mapped.txt
```

Sort and index BAM

```
time samtools sort\  
  mapping/test_mapped.bam\  
  mapping/test_mapped_sorted
```

```
time samtools index\  
  mapping/test_mapped_sorted.bam
```